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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s) : Jean-Christophe RENAULD, et al.
Serial No : 10/026,106
Filed : December 21, 2001
For : ISOLATED CYTOKINE RECEPTOR LICR-2
Art Unit : 1647
Examiner : Fozia M. Hamud

July 22, 2003

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

RESPONSE TO RESTRICTION REQUIREMENT

S I R:

This is submitted in response to the restriction requirement, dated July 14, 2003.

The Examiner has divided the claims into 5 allegedly separable groups. Of these, applicants elect Group I, claims 1-12, 24, 25, and 29.

The Examiner then states that:

"The claims (sic; of) the instant application recite a multitude of nucleic acid and polypeptide sequences (SEQ ID Nos.: 7, 9, 8, and 10). This constitutes a recitation of an implied, mis-joined Markush group that contain multiple, independent and distinct invention. Each of the nucleic acids and polypeptides is independent and distinct because no common structural or functional properties are shared."

These statements, however, are incorrect, and also do not take account of the practice required by the MPEP.

Nucleotide sequence SEQ ID NO: 7 encodes the amino acid sequence of SEQ ID NO: 9. Clearly, the Examiner's comments on distinction and separability are wrong here. Similarly, the nucleotide sequences of SEQ ID NO: 8 encodes the amino acid sequence of SEQ ID NO: 10. Again, any argument regarding distinction is misplaced.

Further, SEQ ID NO: 9 is a splice variant of SEQ ID NO: 7. Please see example 4, at page 6. Note that example 5 discusses experiments which "were designed to check levels of expressions of both LICR-2 isoforms." Clearly, the molecules are related.

Further, SEQ ID NOS.: 8 and 10 are identical through amino acid 177, where 4 amino acids that are present in SEQ ID NO: 8 are missing in SEQ ID NO: 10. There is then sequence identity from amino acid 178/182 through amino acid 223/227. If the amino acids sequences are this closely related, the coding regions must be.

SEQ ID NO: 10 is 244 amino acids long. By definition, then, the coding region of SEQ ID NO: 8 must be 732 nucleotides long. This, given the tremendous degree of identity (not homology) with SEQ ID NOS.: 7 and 9 would immediately suggest complementarity between SEQ ID NOS.: 7 and 8, and thus the ability of SEQ ID NO: 8 to hybridize to a complement of SEQ ID NO: 7 must be taken as a given.

Further, the MPEP is very clear. See MPEP 803.04:

"Nevertheless, to further aid the biotechnology industry the Commissioner has decided...to permit a reasonable number of sequences to be claimed in a single application."

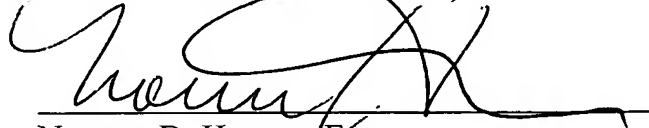
The rule goes on to state that 10 is a reasonable number.

The claims only recite 4 sequences. Clearly, this is within the Commissioner's guidelines.

For the foregoing reasons, the requirement for election of a single sequence should be withdrawn. To complete the response; however, applicants elect SEQ ID NO: 7.

Respectfully submitted,

FULBRIGHT & JAWORSKI, L.L.P.

A handwritten signature in black ink, appearing to read 'Norman D. Hanson', is written over a horizontal line.

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